Listing of claims:

1. (currently amended) A method of identifying a naturally occurring binding partner, or binding partner precursor, for a target, said method comprising:

a) identifying an amino acid sequence motif which confers detectable binding properties of a peptide comprising said motif to a target by screening a library comprising a plurality of different expressed amino acid sequences of from about 20 to about 40 amino acids in length for binding of members of said library to the target; separating members of the library which bind to the target; determining the amino acid sequence of the members of the library which bind to said target; and identifying as motifs common amino acid sequences among said determined amino acid sequences;

b) comparing the identified amino acid sequence motifs to known amino acid sequences of a genome and identifying a gene product of said genome possessing said motif as the naturally occurring binding partner, or partner precursor, for said target.

2. (withdrawn) The method according to claim 1 wherein the target is an untranslated region of mRNA.

3. (withdrawn) The method according to claim 1 wherein the target is a cellular receptor.

4. (original) The method according to claim 1 wherein said library comprises a peptide library of random amino acid sequences.

5 - 6. (canceled)

7. (currently amended) The method according to claim ~~6~~ 4 wherein the random sequence consists essentially of about 20 amino acids.

8. (currently amended) The method according to claim ~~6~~ 4 wherein the random sequence consists essentially of about 40 amino acids.

9. (original) The method according to claim 1 wherein the genome is mammalian.

10. (original) The method according to claim 9 wherein the genome is human.

11. (original) The method according to claim 1 wherein the target is selected from the group consisting of receptors, transport proteins, transcription regulatory sites and translation regulatory sites.

12. (original) The method according to claim 1 wherein the target comprises a protein.

13. (withdrawn) The method according to claim 1 wherein the target comprises a nucleic acid.

14. (withdrawn) The method according to claim 1 wherein the target is a polysaccharide.

15. (original) The method according to claim 1 wherein the motif comprises 5 to 8 amino acids.

16. (original) The method according to claim 15 wherein the common amino acids of said motif are contiguous.

17. (withdrawn) A method of identifying a motif comprising an amino acid sequence of a post translational gene product wherein said motif confers detectable binding properties at a natural target of said post translational gene product, said method comprising screening a library comprising a plurality of different expressed amino acid sequences for binding of members of said library to the target; separating members of the library which bind to the target; determining the amino acid sequence of the members of the library which bind to the target; and identifying as motifs common amino acid sequences among the determined amino acid sequences of said target binding members of the library.

18. (withdrawn) The method according to claim 17 wherein said library comprises a peptide library of random amino acid sequences.

19. (withdrawn) The method according to claim 18 wherein the peptides of said library comprises a random sequence of about 10 to about 50 amino acids.

20. (withdrawn) The method according to claim 19 wherein the random sequence comprises about 20 to 40 amino acids.

21. (withdrawn) The method according to claim 20 wherein the random sequence consists essentially of about 20 amino acids.

22. (withdrawn) The method according to claim 20 wherein the random sequence consists essentially of about 40 amino acids.

23. (withdrawn) The method according to claim 17 wherein said library is a library derived from a primary library by fixing the identity of certain amino acids in known positions of said members of said library.

24. (withdrawn) The method according to claim 17 wherein the common amino acids of said motif are contiguous.

25. (withdrawn) A method for determining the activity of a gene product, said method comprising: a) expressing said gene product in a cell; b) contacting said cells with a ligand which binds said gene product; and c) detecting a change in phenotype of cells in which said gene product is expressed.

26. (withdrawn) The method according to claim 25 wherein said gene product is expressed in a plurality of different cell types.

27. (withdrawn) The method according to claim 25 wherein said ligand possess a consensus amino acid sequence determined from a plurality of members of a peptide library which bind said gene product.

28. (withdrawn) The method according to claim 27 wherein said ligand possesses an amino acid sequence enabling the ligand to enter said cell.

29. (withdrawn) The method according to claim 25 wherein the change in phenotype is detected based on a change in cell growth.

30. (withdrawn) The method according to claim 25 wherein the change in phenotype is detected based on a change in cell morphology.

31. (withdrawn) The method according to claim 25 wherein said ligand is homologous to a natural peptide.

32. (withdrawn) A method of determining the phenotypic outcome of the expression of a gene product comprising; a) expressing the gene product in cells; b) contacting said cells with an amino acid sequence comprising a motif which binds said gene product and wherein said motif is identified from members of a peptide library which bind to the target; and c) detecting a change in phenotype of cells in which said gene product is expressed.

33. (withdrawn) The method according to claim 32 wherein said gene product is expressed in a plurality of different cell types.

34. (withdrawn) The method according to claim 32 wherein said amino acid sequence possesses an amino acid sequence enabling it to enter said cell.

35. (withdrawn) The method according to claim 32 wherein the change in phenotype is detected based on a change in cell growth.

36. (withdrawn) The method according to claim 32 wherein the change in phenotype is detected based on a change in cell morphology.

37. (withdrawn) The method according to claim 32 wherein said motif is present in a naturally occurring gene product.

38. (withdrawn) A method of identifying a naturally occurring binding partner, or binding partner precursor, for a target, said method comprising: a) identifying an amino acid sequence which binds to said target by screening a library comprising a plurality of different expressed amino acid sequences for binding of members of said library to the target; separating at least one member of the library which bind to the target; determining the amino acid sequence of said member of the library which bind to said target; and b) comparing the identified amino acid sequence of said member to known amino acid sequences of a genome and identifying a gene product of said genome possessing an amino acid sequence substantially similar to said identified amino acid sequence as the naturally occurring binding partner, or partner precursor, for said target.

39. (withdrawn) The method according to claim 38 wherein the substantially similar amino acids are identical and contiguous.

40. (withdrawn) The method according to claim 39 wherein at least 5 amino acids are identical and contiguous.

41. (withdrawn) The method according to claim 38 wherein the target is an untranslated region of mRNA.

42. (withdrawn) The method according to claim 38 wherein the target is a cellular receptor.

43. (withdrawn) The method according to claim 38 wherein said library comprises a peptide library of random amino acid sequences.

44. (withdrawn) The method according to claim 43 wherein the peptides of said library comprises a random sequence of about 10 to about 50 amino acids.

45. (withdrawn) The method according to claim 44 wherein the random sequence comprises about 20 to 40 amino acids.

46. (withdrawn) The method according to claim 45 wherein the random sequence consists essentially of about 20 amino acids.

47. (withdrawn) The method according to claim 45 wherein the random sequence consists essentially of about 40 amino acids.

48. (withdrawn) The method according to claim 38 wherein the genome is mammalian.

49. (withdrawn) The method according to claim 48 wherein the genome is human.

50. (withdrawn) The method according to claim 38 wherein the target is selected from the group

consisting of receptors, transport proteins, transcription regulatory sites and translation

regulatory sites.

51. (withdrawn) The method according to claim 38 wherein the target comprises a protein.

52. (withdrawn) The method according to claim 38 wherein the target comprises a nucleic acid.

53. (withdrawn) The method according to claim 38 wherein the target is a polysaccharide.

54. (withdrawn) The method according to claim 38 wherein the motif comprises 5 to 8 amino

acids.

55. (withdrawn) A method for identifying a nucleic acid sequence encoding a naturally occurring

binding partner, or binding partner precursor, for a target, said method comprising: a) identifying

an amino acid sequence motif which confers detectable binding properties of a peptide

comprising said motif to a target by screening a library comprising a plurality of different

expressed amino acid sequences for binding of members of said library to the target; separating

members of the library which bind to the target; determining the amino acid sequence of the members of the library which bind to said target; and identifying as motifs common amino acid sequences among said determined amino acid sequences; b) comparing the identified amino acid sequence motifs to known amino acid sequences of a genome and identifying a gene product of said genome possessing said motif as the naturally occurring binding partner, or partner precursor, for said target; and c) identifying said nucleic acid sequence encoding said naturally occurring binding partner, or partner precursor.

56. (withdrawn) A method of identifying a nucleic acid sequence encoding a naturally occurring binding partner, or binding partner precursor, for a target, said method comprising: a) identifying an amino acid sequence which binds to said target by screening a library comprising a plurality of different expressed amino acid sequences for binding of members of said library to the target; separating at least one member of the library which bind to the target; determining the amino acid sequence of said member of the library which bind to said target; b) comparing the identified amino acid sequence of said member to known amino acid sequences of a genome and identifying a gene product of said genome possessing an amino acid sequence substantially similar to said identified amino acid sequence as the naturally occurring binding partner, or partner precursor, for said target; and c) identifying said nucleic acid sequence encoding said naturally occurring binding partner, or partner precursor.